RAW SEQUENCE LISTING                    DATE: 11/28/2001
PATENT APPLICATION:  US/09/841,805A      TIME: 11:32:06

Input Set : N:\Crf3\RULE60\09841805a.txt
Output Set: N:\CRF3\11282001\I841805A.raw

**SEQUENCE LISTING**

```
 3 (1) GENERAL INFORMATION:
 5      (i) APPLICANT: Lal, Preeti
 6                    Shah, Purvi
 7                    Corley, Neil C.
 9     (ii) TITLE OF INVENTION: HUMAN MEMBRANE RECYCLING
10                             PROTEINS
12    (iii) NUMBER OF SEQUENCES: 5
14     (iv) CORRESPONDENCE ADDRESS:
15          (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
16          (B) STREET: 3174 Porter Dr.
17          (C) CITY: Palo Alto
18          (D) STATE: CA
19          (E) COUNTRY: USA
20          (F) ZIP: 94304
22      (v) COMPUTER READABLE FORM:
23          (A) MEDIUM TYPE: Diskette
24          (B) COMPUTER: IBM Compatible
25          (C) OPERATING SYSTEM: DOS
26          (D) SOFTWARE: FastSEQ for Windows Version 2.0
28     (vi) CURRENT APPLICATION DATA:
C-->29          (A) APPLICATION NUMBER: US/09/841,805A
C-->30          (B) FILING DATE: 24-Apr-2001
31          (C) CLASSIFICATION:
33    (vii) PRIOR APPLICATION DATA:
34          (A) APPLICATION NUMBER: 09/360,125
35          (B) FILING DATE: 1999-07-23
37   (viii) ATTORNEY/AGENT INFORMATION:
38          (A) NAME: Billings, Lucy J.
39          (B) REGISTRATION NUMBER: 36,749
40          (C) REFERENCE/DOCKET NUMBER: PF-0456 US
42     (ix) TELECOMMUNICATION INFORMATION:
43          (A) TELEPHONE: 650-855-0555
44          (B) TELEFAX: 650-845-4166
47 (2) INFORMATION FOR SEQ ID NO: 1:
49      (i) SEQUENCE CHARACTERISTICS:
50          (A) LENGTH: 347 amino acids
51          (B) TYPE: amino acid
52          (C) STRANDEDNESS: single
53          (D) TOPOLOGY: linear
55    (vii) IMMEDIATE SOURCE:
56          (A) LIBRARY: TONGTUT01
57          (B) CLONE: 980615
59     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
61 Met Ala Gln Ser Arg Asp Gly Gly Asn Pro Phe Ala Glu Pro Ser Glu
62  1               5                  10                  15
63 Leu Asp Asn Pro Phe Gln Asp Pro Ala Val Ile Gln His Arg Pro Ser
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64              20              25              30
65   Arg Gln Tyr Ala Thr Leu Asp Val Tyr Asn Pro Phe Glu Thr Arg Glu
66           35              40              45
67   Pro Pro Pro Ala Tyr Glu Pro Pro Ala Pro Ala Pro Leu Pro Pro Pro
68       50              55              60
69   Ser Ala Pro Ser Leu Gln Pro Ser Arg Lys Leu Ser Pro Thr Glu Pro
70   65              70              75              80
71   Lys Asn Tyr Gly Ser Tyr Ser Thr Gln Ala Ser Ala Ala Ala Ala Thr
72               85              90              95
73   Ala Glu Leu Leu Lys Lys Gln Glu Glu Leu Asn Arg Lys Ala Glu Glu
74           100             105             110
75   Leu Asp Arg Arg Glu Arg Glu Leu Gln His Ala Ala Leu Gly Gly Thr
76           115             120             125
77   Ala Thr Arg Gln Asn Asn Trp Pro Pro Leu Pro Ser Phe Cys Pro Val
78       130             135             140
79   Gln Pro Cys Phe Phe Gln Asp Ile Ser Met Glu Ile Pro Gln Glu Phe
80   145             150             155             160
81   Gln Lys Thr Val Ser Thr Met Tyr Tyr Leu Trp Met Cys Ser Thr Leu
82               165             170             175
83   Ala Leu Leu Leu Asn Phe Leu Ala Cys Leu Ala Ser Phe Cys Val Glu
84           180             185             190
85   Thr Asn Asn Gly Ala Gly Phe Gly Leu Ser Ile Leu Trp Val Leu Leu
86           195             200             205
87   Phe Thr Pro Cys Ser Phe Val Cys Trp Tyr Arg Pro Met Tyr Lys Ala
88       210             215             220
89   Phe Arg Ser Asp Ser Ser Phe Asn Phe Phe Val Phe Phe Phe Ile Phe
90   225             230             235             240
91   Phe Val Gln Asp Val Leu Phe Val Leu Gln Ala Ile Gly Ile Pro Gly
92           245             250             255
93   Trp Gly Phe Ser Gly Trp Ile Ser Ala Leu Val Val Pro Lys Gly Asn
94           260             265             270
95   Thr Ala Val Ser Val Leu Met Leu Leu Val Ala Leu Leu Phe Thr Gly
96           275             280             285
97   Ile Ala Val Leu Gly Ile Val Met Leu Lys Arg Ile His Ser Leu Tyr
98       290             295             300
99   Arg Arg Thr Gly Ala Ser Phe Gln Lys Ala Gln Gln Glu Phe Ala Ala
100  305             310             315             320
101  Gly Val Phe Ser Asn Pro Ala Val Arg Thr Ala Ala Ala Asn Ala Ala
102           325             330             335
103  Ala Gly Ala Ala Glu Asn Ala Phe Arg Ala Pro
104           340             345
106  (2) INFORMATION FOR SEQ ID NO: 2:
108         (i) SEQUENCE CHARACTERISTICS:
109             (A) LENGTH: 1521 base pairs
110             (B) TYPE: nucleic acid
111             (C) STRANDEDNESS: single
112             (D) TOPOLOGY: linear
114     (vii) IMMEDIATE SOURCE:
115             (A) LIBRARY: TONGTUT01
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116           (B) CLONE: 980615
118      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
120   NGACGCAGGC GCAACCCACG GCTGCTGCGG GGATCCTTGT GGCCCTTCCG GTCGATGGAA     60
121   CCAATCCGTG CACAGAGAAG CGGGGCGAAC TGAGGCGAGT GAAGTGGACT CTGAGGGCTA    120
122   CCGCTACCGC CACTGCTGCG GCAGGGGCGT GGAGGGCAGA GGGCCGCGGA GGCCGCAGTT    180
123   GCAAACATGG CTCAGAGCAG AGACGGCGGA AACCCGTTCG CCGAGCCCAG CGAGCTTGAC    240
124   AACCCCTTTC AGGACCCAGC TGTGATCCAG CACCGACCCA GCCGGCAGTA TGCCACGCTT    300
125   GACGTCTACA ACCCTTTTGA GACCCGGGAG CCACCACCAG CCTATGAGCC TCCAGCCCCT    360
126   GCCCCATTGC CTCCACCCTC AGCTCCCTCC TTGCAGCCCT CGAGAAAGCT CAGCCCCACA    420
127   GAACCTAAGA ACTATGGCTC ATACAGCACT CAGGCCTCAG CTGCAGCAGC CACAGCTGAG    480
128   CTGCTGAAGA AACAGGAGGA GCTCAACCGG AAGGCAGAGG AGTTGGACCG AAGGGAGCGA    540
129   GAGCTGCAGC ATGCTGCCCT GGGGGGCACA GCTACTCGAC AGAACAATTG GCCCCCTCTA    600
130   CCTTCTTTTT GTCCAGTTCA GCCCTGCTTT TTCCAGGACA TCTCCATGGA GATCCCCCAA    660
131   GAATTTCAGA AGACTGTATC CACCATGTAC TACCTCTGGA TGTGCAGCAC GCTGGCTCTT    720
132   CTCCTGAACT TCCTCGCCTG CCTGGCCAGC TTCTGTGTGG AAACCAACAA TGGCGCAGGC    780
133   TTTGGGCTTT CTATCCTCTG GGTCCTCCTT TTCACTCCCT GCTCCTTTGT CTGCTGGTAC    840
134   CGCCCCATGT ATAAGGCTTT CCGGAGTGAC AGTTCATTCA ATTTCTTCGT TTTCTTCTTC    900
135   ATTTTCTTCG TCCAGGATGT GCTCTTTGTC CTCCAGGCCA TTGGTATCCC AGGTTGGGGA    960
136   TTCAGTGGCT GGATCTCTGC TCTGGTGGTG CCGAAGGGCA ACACAGCAGT ATCCGTGCTC   1020
137   ATGCTGCTGG TCGCCCTGCT CTTCACTGGC ATTGCTGTGC TAGGAATTGT CATGCTGAAA   1080
138   CGGATCCACT CCTTATACCG CCGCACAGGT GCCAGCTTTC AGAAGGCCCA GCAAGAATTT   1140
139   GCTGCTGGTG TCTTCTCCAA CCCTGCGGTG CGAACCGCAG CTGCCAATGC AGCCGCTGGG   1200
140   GCTGCTGAAA ATGCCTTCCG GGCCCCGTGA CCCCTGACTG GGATGCCCTG GCCCTGCTAC   1260
141   TTGAGGGAGC TGACTTAGCT CCCGTCCCTA AGGTCTCTGG GACTTGGAGA GACATCACTA   1320
142   ACTGATGGCT CCTCCGTAGT GCTCCCAATC CTATGGCCAT GACTGCTGAA CCTGACAGGC   1380
143   GTGTGGGGAG TTCACTGTGA CCTAGTCCCC CCATCAGGCC ACACTGCTGC CACCTCTCAC   1440
144   ACGCCCCAAC CCAGCTTCCC TCTGCTGTGC CACGGCTGTT GCTTCGGTTA TTTAAATAAA   1500
145   AAGAAAGTGG AACTGGAACT G                                            1521
147 (2) INFORMATION FOR SEQ ID NO: 3:
149       (i) SEQUENCE CHARACTERISTICS:
150           (A) LENGTH: 329 amino acids
151           (B) TYPE: amino acid
152           (C) STRANDEDNESS: single
153           (D) TOPOLOGY: linear
155     (vii) IMMEDIATE SOURCE:
156           (A) LIBRARY: BRSTNOT01
157           (B) CLONE: 412453
159      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
161   Met Ser Ala Phe Asp Thr Asn Pro Phe Ala Asp Pro Val Asp Val Asn
162   1               5                  10                  15
163   Pro Phe Gln Asp Pro Ser Val Thr Gln Leu Thr Asn Ala Pro Gln Gly
164           20                  25                  30
165   Gly Leu Ala Glu Phe Asn Pro Phe Ser Glu Thr Asn Ala Ala Thr Thr
166           35                  40                  45
167   Val Pro Val Thr Gln Leu Pro Gly Ser Ser Gln Pro Ala Val Leu Gln
168       50                  55                  60
169   Pro Ser Val Glu Pro Thr Gln Pro Thr Pro Gln Ala Val Val Ser Ala
170   65                  70                  75                  80
171   Ala Gln Ala Gly Leu Leu Arg Gln Gln Glu Glu Leu Asp Arg Lys Ala
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172                     85                90                  95
173   Ala Glu Leu Glu Arg Lys Glu Arg Glu Leu Gln Asn Thr Val Ala Asn
174               100               105                 110
175   Leu His Val Arg Gln Asn Asn Trp Pro Pro Leu Pro Ser Trp Cys Pro
176           115               120                 125
177   Val Lys Pro Cys Phe Tyr Gln Asp Phe Ser Thr Glu Ile Pro Ala Asp
178       130               135                 140
179   Tyr Gln Arg Ile Cys Lys Met Leu Tyr Tyr Leu Trp Met Leu His Ser
180   145               150               155                 160
181   Val Thr Leu Phe Leu Asn Leu Leu Ala Cys Leu Ala Trp Phe Ser Gly
182           165               170                 175
183   Asn Ser Ser Lys Gly Val Asp Phe Gly Leu Ser Ile Leu Trp Phe Leu
184           180               185                 190
185   Ile Phe Thr Pro Cys Ala Phe Leu Cys Trp Tyr Arg Pro Ile Tyr Lys
186           195               200                 205
187   Ala Phe Arg Ser Asp Asn Ser Phe Ser Phe Phe Val Phe Phe Phe Val
188       210               215                 220
189   Phe Phe Cys Gln Ile Gly Ile Tyr Ile Ile Gln Leu Val Gly Ile Pro
190   225               230               235                 240
191   Gly Leu Gly Asp Ser Gly Trp Ile Ala Ala Leu Ser Thr Leu Asp Asn
192           245               250                 255
193   His Ser Leu Ala Ile Ser Val Ile Met Met Val Val Ala Gly Phe Phe
194           260               265                 270
195   Thr Leu Cys Ala Val Leu Ser Val Phe Leu Leu Gln Arg Val His Ser
196           275               280                 285
197   Leu Tyr Arg Arg Thr Gly Ala Ser Phe Gln Gln Ala Gln Glu Glu Phe
198       290               295                 300
199   Ser Gln Gly Ile Phe Ser Ser Arg Thr Phe His Arg Ala Ala Ser Ser
200   305               310               315                 320
201   Ala Ala Gln Gly Ala Phe Gln Gly Asn
202                     325
204 (2) INFORMATION FOR SEQ ID NO: 4:
206       (i) SEQUENCE CHARACTERISTICS:
207             (A) LENGTH: 2434 base pairs
208             (B) TYPE: nucleic acid
209             (C) STRANDEDNESS: single
210             (D) TOPOLOGY: linear
212      (vii) IMMEDIATE SOURCE:
213             (A) LIBRARY: BRSTNOT01
214             (B) CLONE: 412453
216      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
218  NCCGGAAGTG GAGGGTCTAC ACGAAGCGCC GCTGGGTCTG GGTGCCCGGA GGCAGCAGCG      60
219  TTCGCGGAGT TCGCCCGCTG GCCCCCGATC ACCATGTCGG CTTTCGACAC CAACCCCTTC     120
220  GCGGACCCAG TGGATGTAAA CCCCTTCCAG GATCCCTCTG TGACCCAGCT GACCAACGCC     180
221  CCGCAGGGCG GCCTGGCGGA ATTCAACCCC TTCTCAGAGA CAAATGCAGC GACAACAGTT     240
222  CCTGTCACCC AACTCCCTGG GTCCTCACAG CCAGCGGTTC TCCAGCCATC AGTGGAACCA     300
223  ACCCAGCCGA CCCCCCAGGC CGTGGTGTCT GCAGCCCAGG CAGGCCTGCT CCGGCAGCAG     360
224  GAAGAACTGG ACAGGAAAGC TGCCGAGCTG GAACGCAAGG AGCGGGAGCT GCAGAACACT     420
225  GTAGCCAACT TGCATGTGAG ACAGAACAAC TGGCCCCCTC TGCCCTCGTG GTGCCCTGTG     480
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RAW SEQUENCE LISTING
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226  AAGCCCTGCT TCTATCAGGA TTTCTCCACA GAGATCCCTG CCGACTACCA GCGGATATGC   540
227  AAGATGCTCT ACTATCTGTG GATGTTGCAT TCAGTGACTC TGTTTCTGAA CCTGCTTGCC   600
228  TGCCTGGCCT GGTTCTCGGG CAACAGCTCC AAGGGAGTGG ACTTTGGCCT CTCCATCCTG   660
229  TGGTTTCTGA TCTTCACTCC CTGTGCCTTC CTTTGTTGGT ACCGACCCAT CTATAAGGCC   720
230  TTTAGGTCCG ACAACTCTTT CAGCTTCTTT GTGTTCTTCT TTGTATTTTT TTGTCAAATA   780
231  GGGATCTACA TCATCCAGTT GGTTGGCATC CCTGGCCTGG GGACAGCGG TTGGATTGCA   840
232  GCCCTGTCTA CACTGGATAA TCATTCCCTG GCCATATCAG TCATCATGAT GGTGGTGGCT   900
233  GGCTTCTTCA CCCTCTGTGC CGTGCTCTCA GTCTTCCTCC TGCAGCGGGT GCACTCCCTC   960
234  TACCGACGGA CAGGGGCCAG CTTCCAGCAG GCCCAGGAGG AGTTTTCCCA GGGCATCTTC  1020
235  AGCAGCAGAA CCTTCCACAG AGCTGCTTCA TCTGCTGCCC AAGGAGCCTT CCAGGGGAAT  1080
236  TAGTCCTCCT CTCTTCTCTC CCCCTCAGCC TTTCTCTCGC CTGCCTTCTG AGCTGCACTT  1140
237  TCCGTGGGTG CCTTATGTGG TGGTGGTTGT GCCCAGCACA GACCTGGCAG GGTTCTTGCC  1200
238  GTGGCTCTTC CTCCTCCCTC AGCGACCAGC TCTCCCTGGA ACGGGAGGGA CAGGGAATTT  1260
239  TTTCCCCCTC TATGTACAAA AAAAAACAAA GCTCTCTTTC CTTCTCTGGT GATGGTTTGG  1320
240  TAGGATTCTT TTGTCTCTGG AAGCAGTGGG ACTGAAGTTC TCTTCGTCCT GTGCACACAC  1380
241  AGACACCCCC ACACAGTTGG GATCACAGGC TGACCTGGGC CCATCCCAGC TGGAGCTTTC  1440
242  TGCCAGGGTC CTGGGCCTTG ACTCCCCCAC CCTGCAGGCC TGGCCTGAAT CTGGCTTCTT  1500
243  AGACACAGCC CAGTCCTTCC TGCCTGGGCT GGGAATAAGC CTCTCACAGG TTCTGGTGGA  1560
244  CAGATCTGTT CCCCAGGTCA CTCCAGTGGT CTCCAGGCTT CCAGAGAAGG CTGGTTGCCT  1620
245  CAAGCTCTTC TCTGCCTCAT AAACGGATCC AGAGAAGGCT GGTTGCCTTA AGCTCTTCCC  1680
246  TGCCTCGTGT TCCTGAGAAA CGGATTAATA GCCCTTTATC CCCCTGCACC CTCCTGCAGG  1740
247  GGATGGCACT TTGAGCCCTC TGGAGCCCTC CCCTTGCTGA GCCTTACTCT CTTCAGACTT  1800
248  TCTGAATGTA CAGTGCCGTT GGTTGGGATT TGGGGACTGG AAGGGACCAA GGACACTGAC  1860
249  CCCAAGCTGT CCTGCCTAGC GTCCAGCGTC TTCTAGGAGG GTGGGGTCTG CCTGTCCTGG  1920
250  TGTGGTTGGT TTGGCCCTGT TTGCTGTGAC TACCCCCCCC CCTCCCCGAA CCGAGGGACG  1980
251  GCTGCCTTTG TCTCTGCCTC AGATGCCACC TGCCCCGCCC ATGCTCCCCA TCAGCAGCAT  2040
252  CCAGACTTTC AGGAAGGGCA GGACCAGCCA GTCCAGAACC GCATCCCTCA GCAGGGACTG  2100
253  ATAAGCCATC TCTCGGAGGG CCCCCTAATA CCCAGTGGAG TCTGGTTCAC ACCCTGGGGG  2160
254  GTGTGTCACT GTGATGGGAC ACGTAGGAGT CCACCCTTAA AACCAGCACC CTGTCCCTCG  2220
255  AGGCTGCCGA GTGGGTGTGT GGACTGGGGT GCCTTCCCAC AAAACTAGCC TCCGGCTCTG  2280
256  GGCCCGAGAC AGCCGCAGGC CCCAGCCACT GAATGATACT GGCAGCGGCT GGGGTTTTAT  2340
257  GAACTCCTTT CTGGTATTTT TTCCCCTCTA TGTACAAATG TATATGTTAC GTCTCAATTT  2400
258  TTGTGCTTAA GTAAAAATAA AAACATTTTC AGAC                              2434
260  (2) INFORMATION FOR SEQ ID NO: 5:
262       (i) SEQUENCE CHARACTERISTICS:
263           (A) LENGTH: 338 amino acids
264           (B) TYPE: amino acid
265           (C) STRANDEDNESS: single
266           (D) TOPOLOGY: linear
268     (vii) IMMEDIATE SOURCE:
269           (A) LIBRARY: GenBank
270           (B) CLONE: 487057
272      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
274  Met Ser Asp Phe Asp Ser Asn Pro Phe Ala Asp Pro Asp Leu Asn Asn
275  1               5                  10                  15
276  Pro Phe Lys Asp Pro Ser Val Thr Gln Val Thr Arg Asn Val Pro Pro
277              20                  25                  30
278  Gly Leu Asp Glu Tyr Asn Pro Phe Ser Asp Ser Arg Thr Pro Pro Pro
279              35                  40                  45
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**VERIFICATION SUMMARY**          DATE: 11/28/2001
PATENT APPLICATION:  US/09/841,805A       TIME: 11:32:07

Input Set : **N:\Crf3\RULE60\09841805a.txt**
Output Set: **N:\CRF3\11282001\I841805A.raw**

L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]